

AATTCGTTCT ACCTTCTCTG AACCCCAAGTG GTGTGTCAAG GCCGGACTGG GAGCTTGGGG 60  
GAAGAGGAAG AGGAAGAGGA ATCTGCGGCT CATCCAGGGA TCAGGGTCCT TCCCAAGTGG 120  
CCACTCAGAG GGGACTCAGA GCAAGTCTAG ATTTGTGTGG CAGAGAGAGA CAGCTCTCGT 180  
TTGGCCTTGG GGAGGCACAA GTCTGTTGAT AACCTGAAGA CA 222  
  
ATG GAT GTC GAT GAG GGT CAA GAC ATG TCC CAA GTT TCA GGA AAG GAG 270  
Met Asp Val Asp Glu Gly Gln Asp Met Ser Gln Val Ser Gly Lys Glu  
1 5 10 15  
  
AGC CCC CCA GTC AGT GAC ACT CCA GAT GAA GGG GAT GAG CCC ATG CCT 318  
Ser Pro Pro Val Ser Asp Thr Pro Asp Glu Gly Asp Glu Pro Met Pro  
20 25 30  
  
GTC CCT GAG GAC CTG TCC ACT ACC TCT GGA GCA CAG CAG AAC TCC AAG 366  
Val Pro Glu Asp Leu Ser Thr Thr Ser Gly Ala Gln Gln Asn Ser Lys  
35 40 45  
  
AGT GAT CGA GGC ATG GGT GAA CGG CCT TTC CAG TGC AAC CAG TCT GGG 414  
Ser Asp Arg Gly Met Gly Gln Arg Pro Phe Gln Cys Asn Gln Ser Gly  
50 55 60  
  
GCC TCC TTT ACC CAG AAA GGC AAC CTC CTG CGG CAC ATC AAG CTG CAC 462  
Ala Ser Phe Thr Gln Lys Gly Asn Leu Leu Arg His Ile Lys Leu His  
65 70 75 80  
  
TCG GGT GAG AAG CCC TTC AAA TGC CAT CTT TGC AAC TAT GCC TGC CGC 510  
Ser Gly Glu Lys Pro Phe Lys Cys His Leu Cys Asn Tyr Ala Cys Arg  
85 90 95  
  
CGG AGG GAC GCC CTC ACC GGC CAC CTG AGG ACG CAC TCC GTT GGT AAG 558  
Arg Arg Asp Ala Leu Thr Gly His Leu Arg Thr His Ser Val Gly Lys  
100 105 110  
  
CCT CAC AAA TGT GGA TAT TGT GGC CGG AGC TAT AAA CAG CGA AGC TCT 606  
Pro His Lys Cys Gly Tyr Cys Gly Arg Ser Tyr Lys Gln Arg Ser Ser  
115 120 125  
  
TTA GAG GAG CAT AAA GAG CGA TGC CAC AAC TAC TTG GAA AGC ATG GGC 654  
Leu Glu Glu His Lys Glu Arg Cys His Asn Tyr Leu Glu Ser Met Gly  
130 135 140  
  
CTT CCG GGC GTG TGC CCA GTC ATT AAG GAA GAA ACT AAC CAC AAC GAG 702  
Leu Pro Gly Val Cys Pro Val Ile Lys Glu Glu Thr Asn His Asn Glu  
145 150 155 160  
  
ATG GCA GAA GAC CTG TGC AAG ATA GGA GCA GAG AGG TCC CTT GTC CTG 750  
Met Ala Glu Asp Leu Cys Lys Ile Gly Ala Glu Arg Ser Leu Val Leu  
165 170 175  
  
GAC AGG CTG GCA AGC AAT GTC GCC AAA CGT AAG AGC TCT ATG CCT CAG 798  
Asp Arg Leu Ala Ser Asn Val Ala Lys Arg Lys Ser Ser Met Pro Gln  
180 185 190

FIG. 1A

AAA TTT CTT GGA GAC AAG TGC CTG TCA GAC ATG CCC TAT GAC AGT GCC	846
Lys Phe Leu Gly Asp Lys Cys Leu Ser Asp Met Pro Tyr Asp Ser Ala	
195 200 205	
AAC TAT GAG AAG GAG GAT ATG ATG ACA TCC CAC GTG ATG GAC CAG GCC	894
Asn Tyr Glu Lys Glu Asp Met Met Thr Ser His Val Met Asp Gln Ala	
210 215 220	
ATC AAC AAT GCC ATC AAC TAC CTG GGG GCT GAG TCC CTG CGC CCA TTG	942
Ile Asn Asn Ala Ile Asn Tyr Leu Gly Ala Glu Ser Leu Arg Pro Leu	
225 230 235 240	
GTG CAG ACA CCC CCC GGT AGC TCC GAG GTG GTG CCA GTC ATC AGC TCC	990
Val Gln Thr Pro Pro Gly Ser Ser Glu Val Val Pro Val Ile Ser Ser	
245 250 255	
ATG TAC CAG CTG CAC AAG CCC CCC TCA GAT GGC CCC CCA CGG TCC AAC	1038
Met Tyr Gln Leu His Lys Pro Pro Ser Asp Gly Pro Pro Arg Ser Asn	
260 265 270	
CAT TCA GCA CAG GAC GCC GTG GAT AAC TTG CTG CTG CTG TCC AAG GCC	1086
His Ser Ala Gln Asp Ala Val Asp Asn Leu Leu Leu Leu Ser Lys Ala	
275 280 285	
AAG TCT GTG TCA TCG GAG CGA GAG GCC TCC CCG AGC AAC AGC TGC CAA	1134
Lys Ser Val Ser Ser Glu Arg Glu Ala Ser Pro Ser Asn Ser Cys Gln	
290 295 300	
GAC TCC ACA GAT ACA GAG AGC AAC GCG GAG GAA CAG CGC AGC GGC CTT	1182
Asp Ser Thr Asp Thr Glu Ser Asn Ala Glu Glu Gln Arg Ser Gly Leu	
305 310 315 320	
ATC TAC CTA ACC AAC CAC ATC AAC CCG CAT GCA CGC AAT GGG CTG GCT	1230
Ile Tyr Leu Thr Asn His Ile Asn Pro His Ala Arg Asn Gly Leu Ala	
325 330 335	
CTC AAG GAG GAG CAG CGC GCC TAC GAG GTG CTG AGG GCG GCC TCA GAG	1278
Leu Lys Glu Glu Gln Arg Ala Tyr Glu Val Leu Arg Ala Ala Ser Glu	
340 345 350	
AAC TCG CAG GAT GCC TTC CGT GTG GTC AGC ACG AGT GGC GAG CAG CTG	1326
Asn Ser Gln Asp Ala Phe Arg Val Val Ser Thr Ser Gly Glu Gln Leu	
355 360 365	
AAG GTG TAC AAG TGC GAA CAC TGC CGC GTG CTC TTC CTG GAT CAC GTC	1374
Lys Val Tyr Lys Cys Glu His Cys Arg Val Leu Phe Leu Asp His Val	
370 375 380	
ATG TAT ACC ATT CAC ATG GGC TGC CAT GGC TGC CAT GGC TTT CGG GAT	1422
Met Tyr Thr Ile His Met Gly Cys His Gly Cys His Gly Phe Arg Asp	
385 390 395 400	
CCC TTT GAG TGT AAC ATG TGT GGT TAT CAC AGC CAG GAC AGG TAC GAG	1470
Pro Phe Glu Cys Asn Met Cys Gly Tyr His Ser Gln Asp Arg Tyr Glu	
405 410 415	

FIG. 1B

TTC TCA TCC CAT ATC ACG CGG GGG GAG CAT CGT TAC CAC CTG AGC	1515
Phe Ser Ser His Ile Thr Arg Gly Glu His Arg Tyr His Leu Ser	
420 425 430	
TAAACCCAGC CAGGCCCCAC TGAAGCACAA AGATAGCTGG TTATGCCTCC TTCCCGGCAG	1575
CTGGACCCAC AGCGGACAAT GTGGGAGTGG ATTTGCAGGC AGCATTGTGT CTTTATGTGT	1635
GGTTGTTTGG CGTTTCATTT GCGTTGGAAG ATAAGTTTTT AATGTTAGTG ACAGGATTGC	1695
ATTGCATCAG CAACATTCAC AACATCCATC CTTCTAGCCA GTTTTGTTCA CTGGTAGCTG	1755
AGGTTTCCCG GATATGTGGC TTCCTAACAC TCT	1788

(SEQ.ID.NO:1)

FIG. 1C

AAT GTT AAA GTA GAG ACT CAG AGT GAT GAA GAG AAT GGG CGT GCC TGT	48
Asn Val Lys Val Glu Thr Gln Ser Asp Glu Glu Asn Gly Arg Ala Cys	
1 5 10 15	
GAA ATG AAT GGG GAA GAA TGT GCG GAG GAT TTA CGA ATG CTT GAT GCC	96
Glu Met Asn Gly Glu Glu Cys Ala Glu Asp Leu Arg Met Leu Asp Ala	
20 25 30	
TCG GGA GAG AAA ATG AAT GGC TCC CAC AGG GAC CAA GGC AGC TCG GCT	144
Ser Gly Glu Lys Met Asn Gly Ser His Arg Asp Gln Gly Ser Ser Ala	
35 40 45	
TTG TCG GGA GTT GGA GGC ATT CGA CTT CCT AAC GGA AAA CTA AAG TGT	192
Leu Ser Gly Val Gly Gly Ile Arg Leu Pro Asn Gly Lys Leu Lys Cys	
50 55 60	
GAT ATC TGT GGG ATC ATT TGC ATC GGG CCC AAT GTG CTC ATG GTT CAC	240
Asp Ile Cys Gly Ile Ile Cys Ile Gly Pro Asn Val Leu Met Val His	
65 70 75 80	
AAA AGA AGC CAC ACT GGA GAA CGG CCC TTC CAG TGC AAT CAG TGC GGG	288
Lys Arg Ser His Thr Gly Glu Arg Pro Phe Gln Cys Asn Gln Cys Gly	
85 90 95	
GCC TCA TTC ACC CAG AAG GGC AAC CTG CTC CGG CAC ATC AAG CTG CAT	336
Ala Ser Phe Thr Gln Lys Gly Asn Leu Arg His Ile Lys Leu His	
100 105 110	
TCC GGG GAG AAG CCC TTC AAA TGC CAC CTC TGC AAC TAC GCC TGC CGC	384
Ser Gly Glu Lys Pro Phe Lys Cys His Leu Cys Asn Tyr Ala Cys Arg	
115 120 125	
CGG AGG GAC GCC CTC ACT GGC CAC CTG AGG ACG CAC TCC GTT GGT AAA	432
Arg Arg Asp Ala Leu Thr Gly His Leu Arg Thr His Ser Val Gly Lys	
130 135 140	
CCT CAC AAA TGT GGA TAT TGT GGC CGA AGC TAT AAA CAG CGA ACG TCT	480
Pro His Lys Cys Gly Tyr Cys Gly Arg Ser Tyr Lys Gln Arg Thr Ser	
145 150 155 160	
TTA GAG GAA CAT AAA GAG CGC TGC CAC AAC TAC TTG GAA AGC ATG GGC	528
Leu Glu Glu His Lys Glu Arg Cys His Asn Tyr Leu Glu Ser Met Gly	
165 170 175	
CTT CCG GGC ACA CTG TAC CCA GTC ATT AAA GAA GAA ACT AAG CAC AGT	576
Leu Pro Gly Thr Leu Tyr Pro Val Ile Lys Glu Glu Thr Lys His Ser	
180 185 190	
GAA ATG GCA GAA GAC CTG TGC AAG ATA GGA TCA GAG AGA TCT CTC GTG	624
Glu Met Ala Glu Asp Leu Cys Lys Ile Gly Ser Glu Arg Ser Leu Val	
195 200 205	
CTG GAC AGA CTA GCA AGT AAT GTC GCC AAA CGT AAG AGC TCT ATG CCT	672
Leu Asp Arg Leu Ala Ser Asn Val Ala Lys Arg Lys Ser Ser Met Pro	
210 215 220	
CAG AAA TTT CTT GGG GAC AAG GGC CTG TCC GAC ACG CCC TAC GAC AGT	720
Gln Lys Phe Leu Gly Asp Lys Gly Leu Ser Asp Thr Pro Tyr Asp Ser	
225 230 235 240	

FIG. 2A

GCC ACG TAC GAG AAG GAG AAC GAA ATG ATG AAG TCC CAC GTG ATG GAC	768
Ala Thr Tyr Glu Lys Glu Asn Glu Met Met Lys Ser His Val Met Asp	
245 250 255	
CAA GCC ATC AAC AAC GCC ATC AAC TAC CTG GGG GCC GAG TCC CTG CGC	816
Gln Ala Ile Asn Asn Ala Ile Asn Tyr Leu Gly Ala Glu Ser Leu Arg	
260 265 270	
CCG CTG GTG CAG ACG CCC CCG GGC GGT TCC GAG GTG GTC CCG GTC ATC	864
Pro Leu Val Gln Thr Pro Pro Gly Gly Ser Glu Val Val Pro Val Ile	
275 280 285	
AGC CCG ATG TAC CAG CTG CAC AGG CGC TCG GAG GGC ACC CCG CGC TCC	912
Ser Pro Met Tyr Gln Leu His Arg Arg Ser Glu Gly Thr Pro Arg Ser	
290 295 300	
AAC CAC TCG GCC CAG GAC AGC GCC GTG GAG TAC CTG CTG CTG CTC TCC	960
Asn His Ser Ala Gln Asp Ser Ala Val Glu Tyr Leu Leu Leu Leu Ser	
305 310 315 320	
AAG GCC AAG TTG GTG CCC TCG GAG CGC GAG GCG TCC CCG AGC AAC AGC	1008
Lys Ala Lys Leu Val Pro Ser Glu Arg Glu Ala Ser Pro Ser Asn Ser	
325 330 335	
TGC CAA GAC TCC ACG GAC ACC GAG AGC AAC AAC GAG GAG CAG CGC AGC	1056
Cys Gln Asp Ser Thr Asp Thr Glu Ser Asn Asn Glu Glu Gln Arg Ser	
340 345 350	
GGT CTT ATC TAC CTG ACC AAC CAC ATC GCC CGA CGC GCG CAA CGC GTG	1104
Gly Leu Ile Tyr Leu Thr Asn His Ile Ala Arg Arg Ala Gln Arg Val	
355 360 365	
TCG CTC AAG GAG GAG CAC CGC GCC TAC GAC CTG CTG CGC GCC GCC TCC	1152
Ser Leu Lys Glu Glu His Arg Ala Tyr Asp Leu Leu Arg Ala Ala Ser	
370 375 380	
GAG AAC TCG CAG GAC GCG CTC CGC GTG GTC AGC ACC AGC GGG GAG CAG	1200
Glu Asn Ser Gln Asp Ala Leu Arg Val Val Ser Thr Ser Gly Glu Gln	
385 390 395 400	
ATG AAG GTG TAC AAG TGC GAA CAC TGC CGG GTG CTC TTC CTG GAT CAC	1248
Met Lys Val Tyr Lys Cys Glu His Cys Arg Val Leu Phe Leu Asp His	
405 410 415	
GTC ATG TAC ACC ATC CAC ATG GGC TGC CAC GGC TTC CGT GAT CCT TTT	1296
Val Met Tyr Thr Ile His Met Gly Cys His Gly Phe Arg Asp Pro Phe	
420 425 430	
GAG TGC AAC ATG TGC GGC TAC CAC AGC CAG GAC CGG TAC GAG TTC TCG	1344
Glu Cys Asn Met Cys Gly Tyr His Ser Gln Asp Arg Tyr Glu Phe Ser	
435 440 445	
TCG CAC ATA ACG CGA GGG GAG CAC CGC TTC CAC ATG AGC TAA	1386
Ser His Ile Thr Arg Gly Glu His Arg Phe His Met Ser	
450 455 460	

(SEQ.ID.NO:2)

FIG. 2B

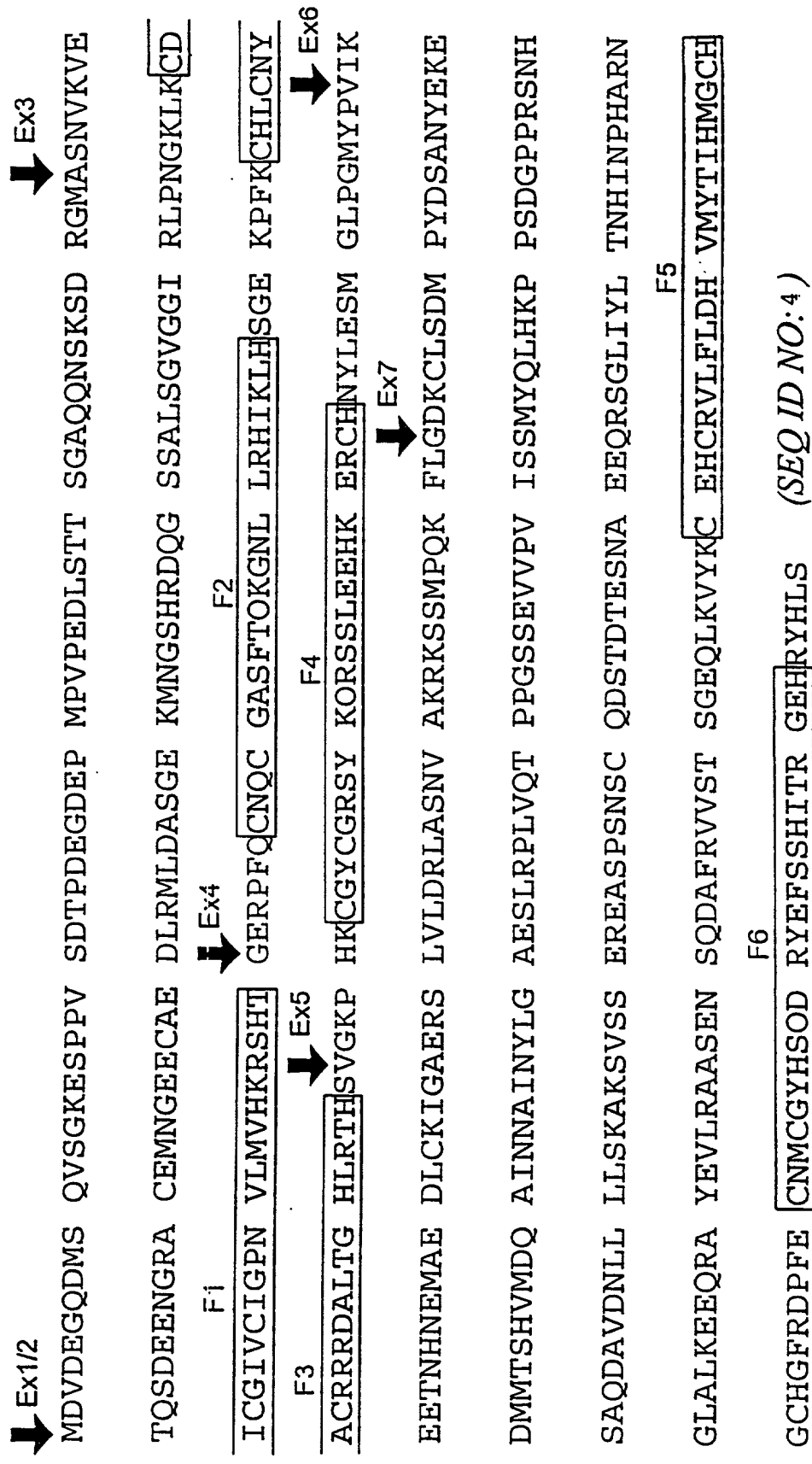


FIG. 3

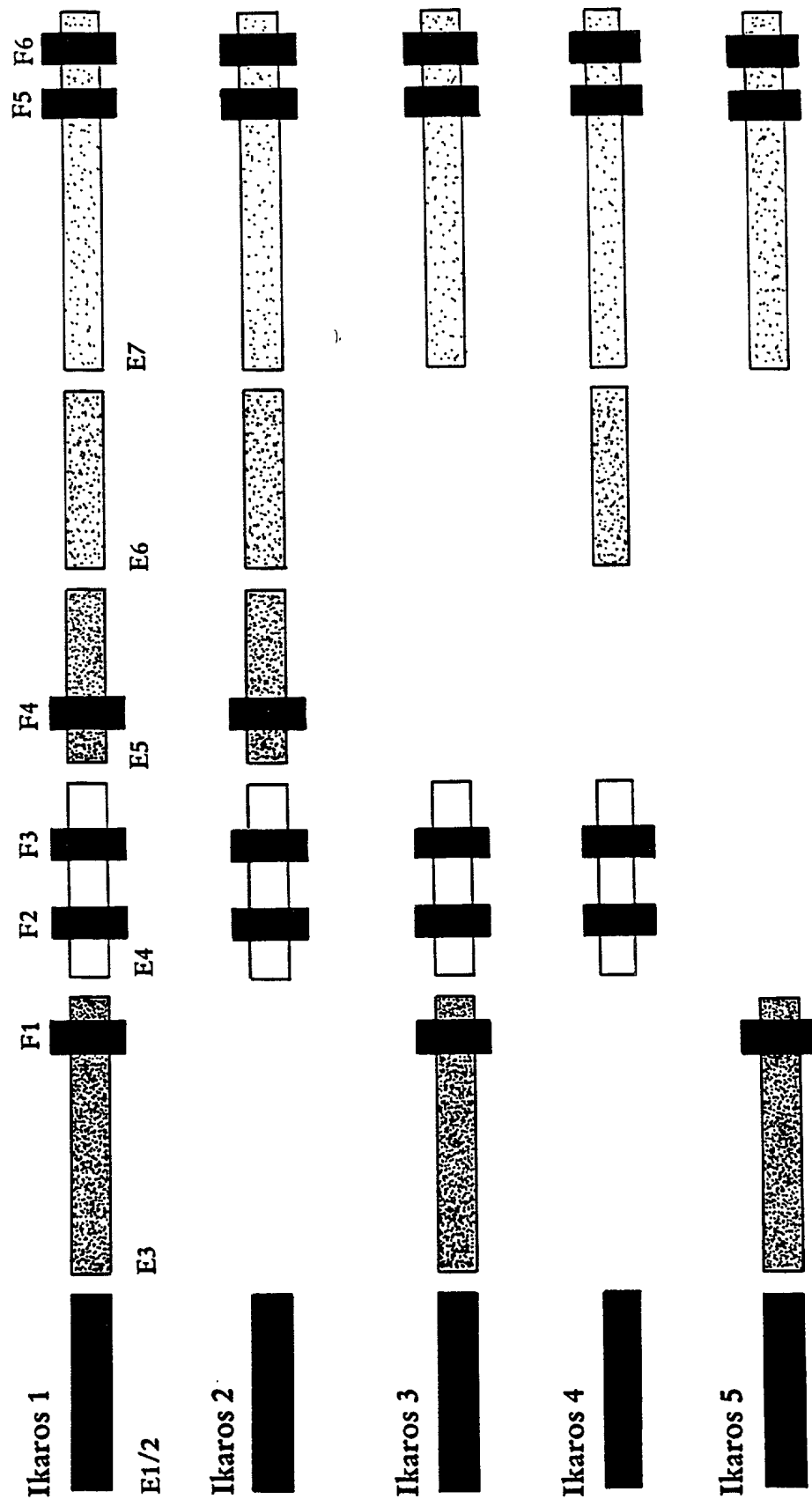
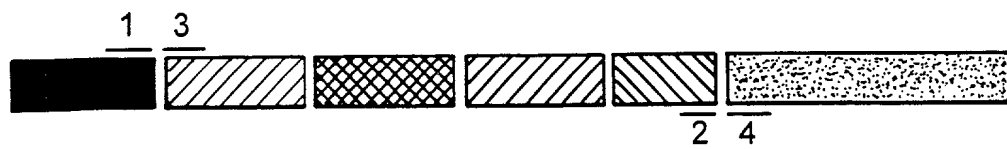


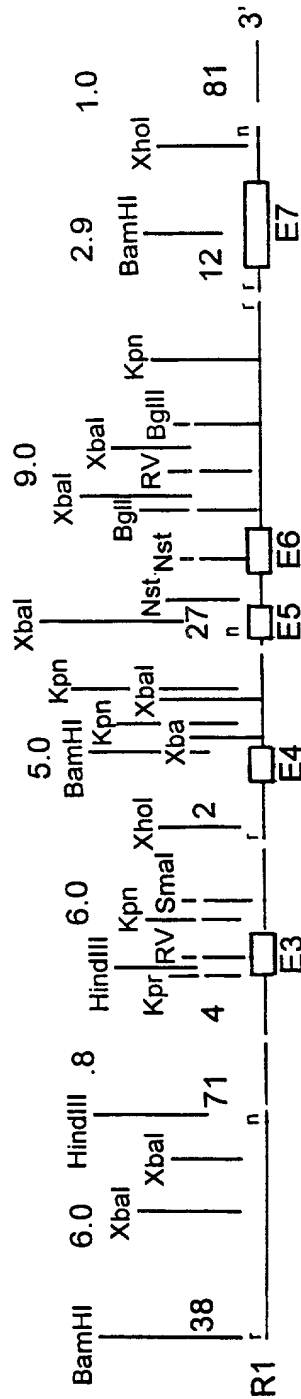
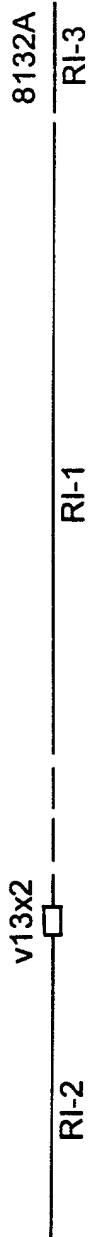
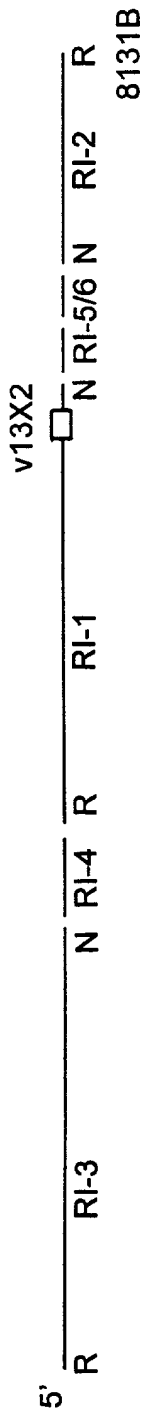
FIG. 4



Oligo1/2 IK-1/IK-2/IK-4

Oligo3/4 IK-1/IK-3/IK-5

FIG. 5



2kb

f2

f10

f4

f8

FIG. 6

# An Ikaros view of the hemopoietic system; expression and potential roles in development

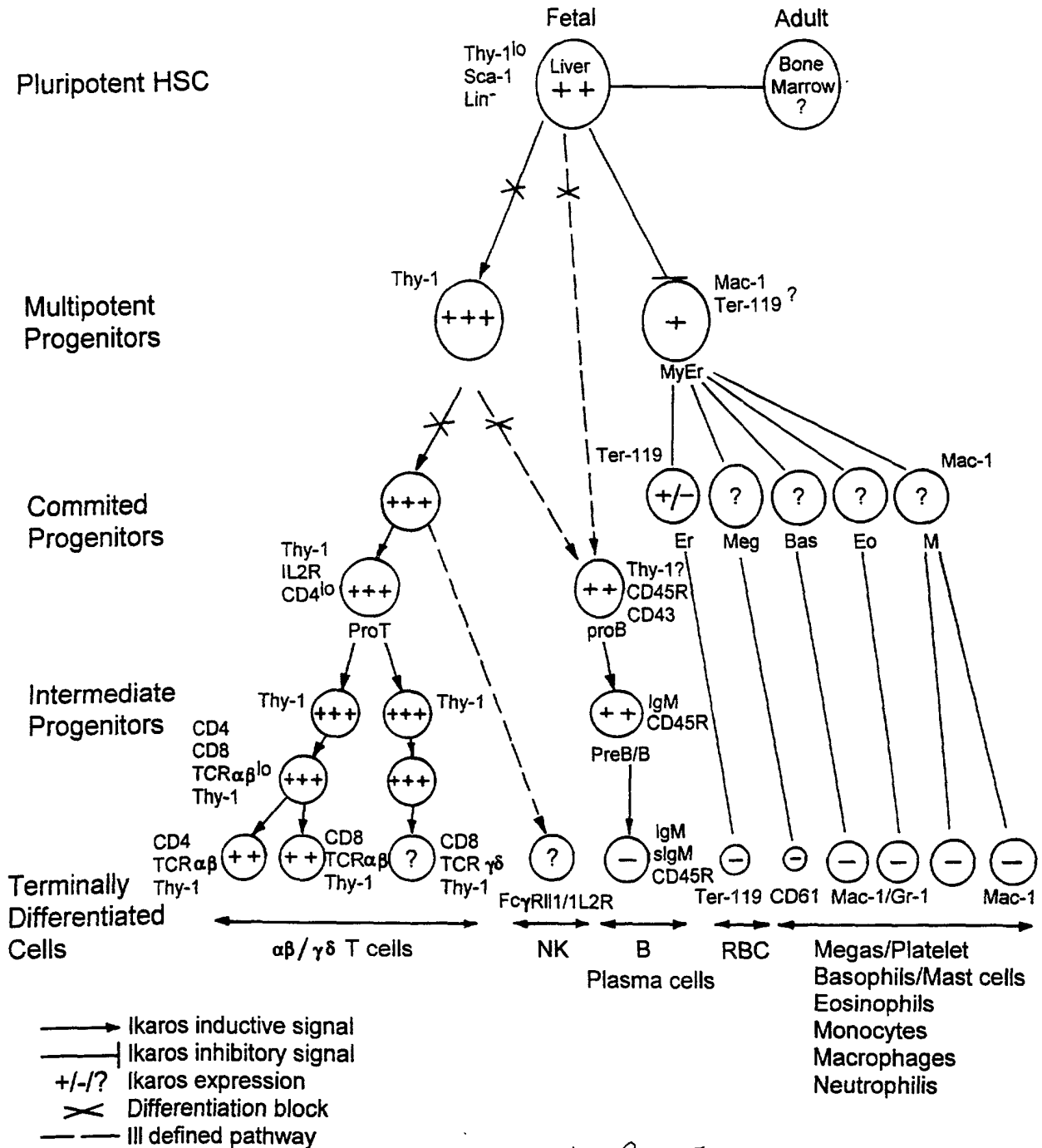


FIG. 7

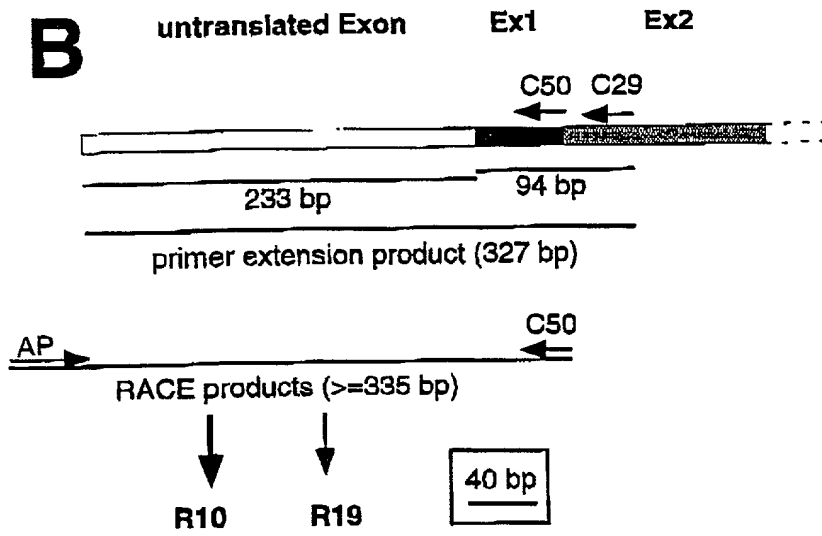
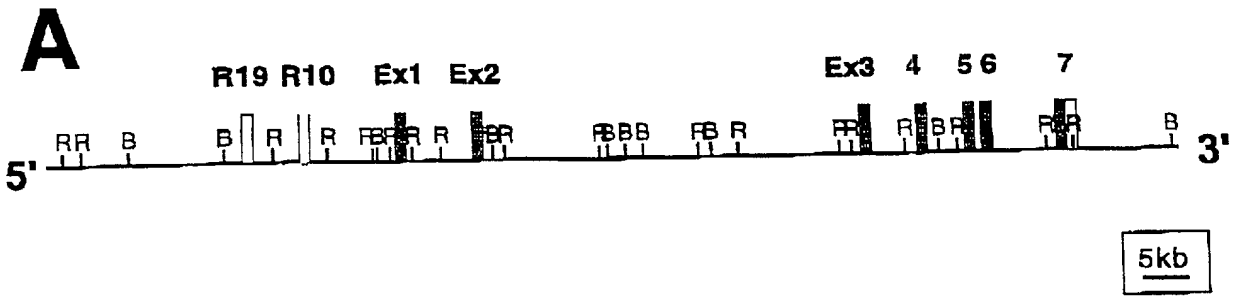


FIG. 8

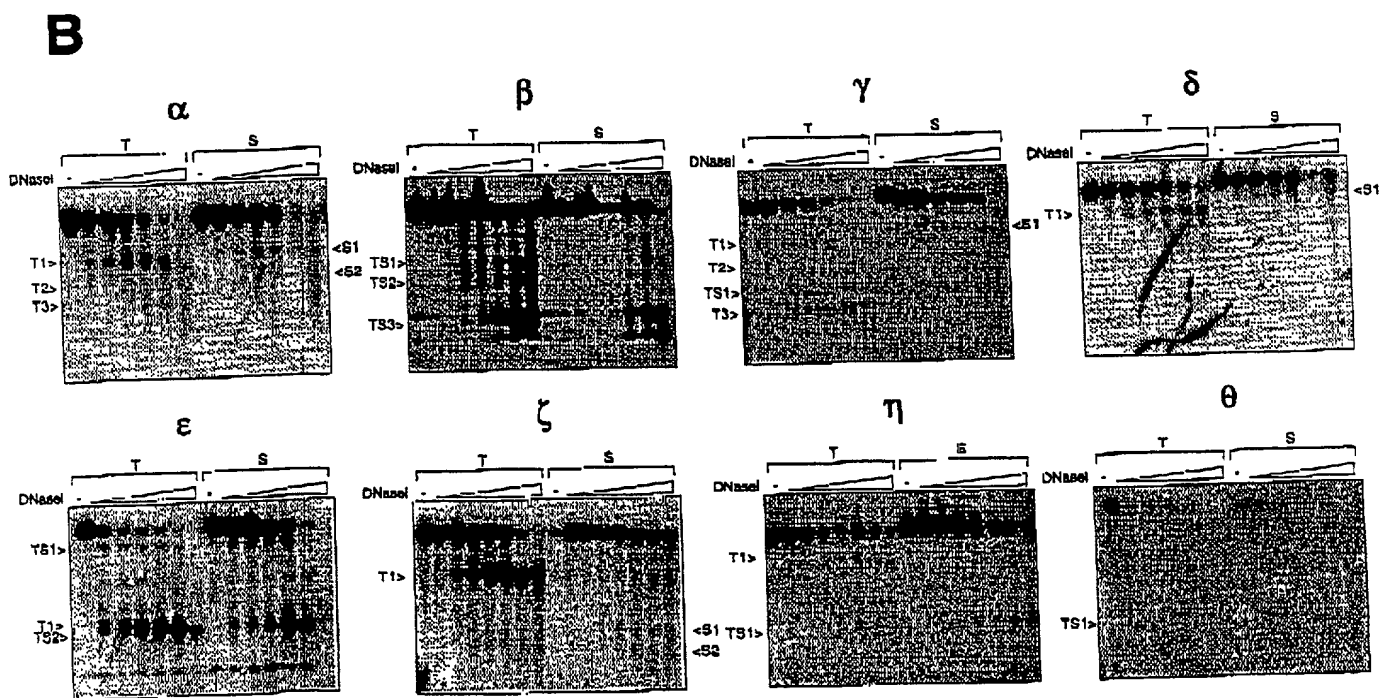
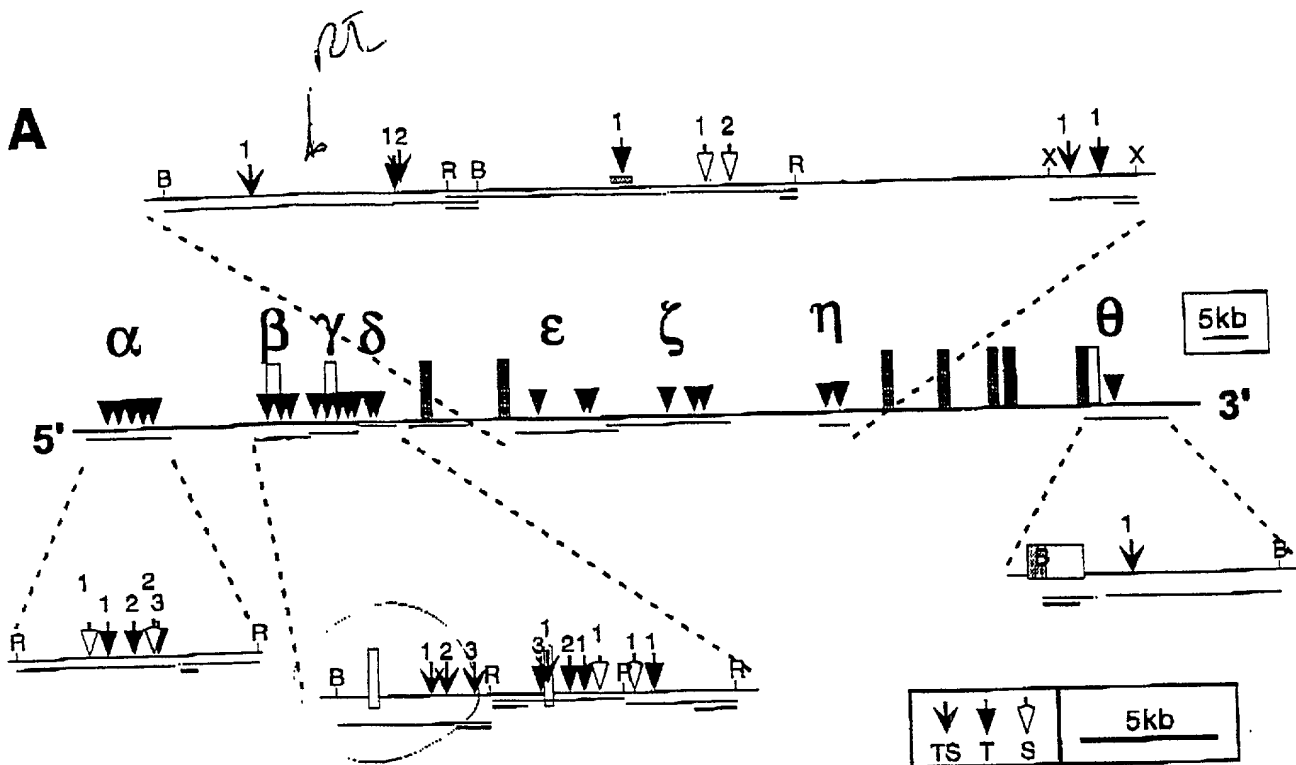


FIG. 9

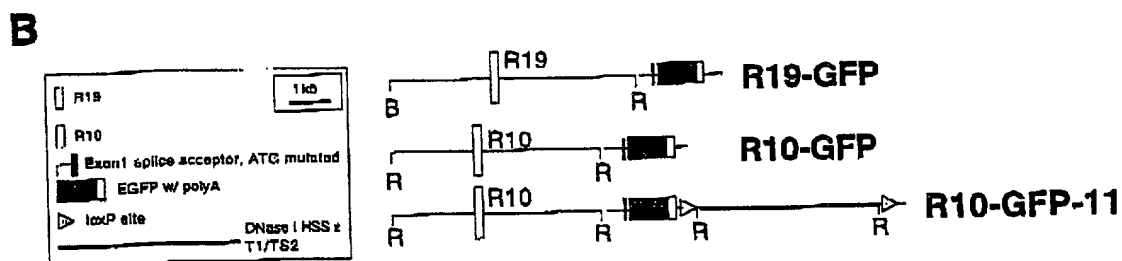
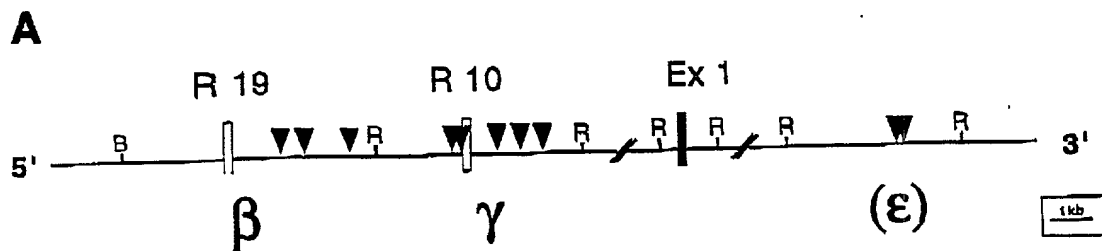
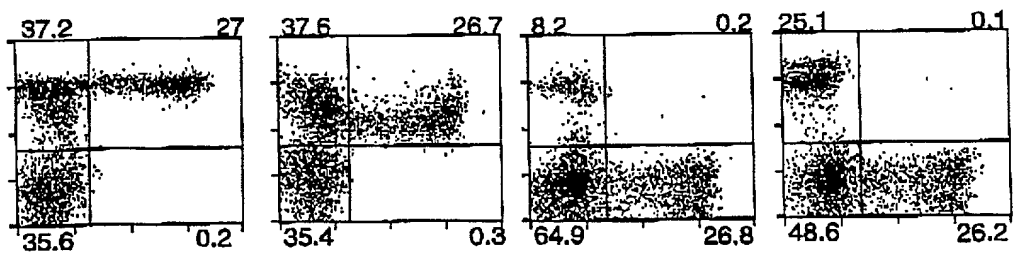


FIG. 10

## Bone Marrow

### R19-GFP



### R10-GFP

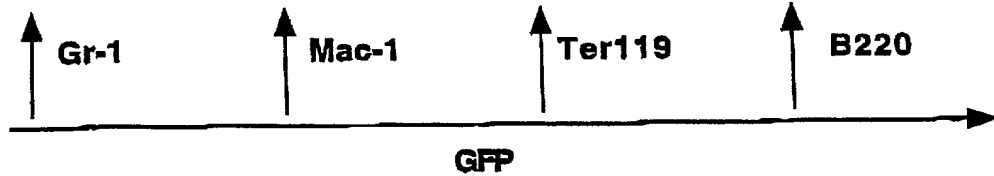
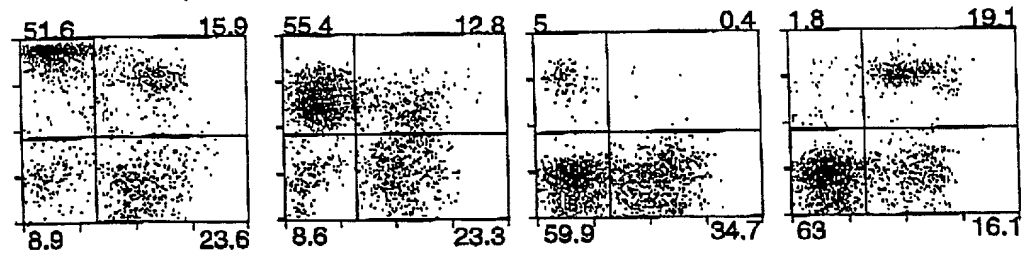
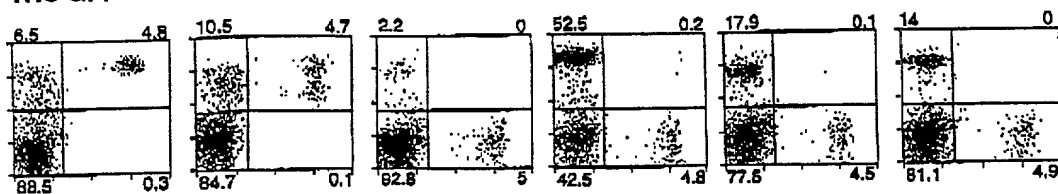


FIG. 11

# Spleen

## R19-GFP



## R10-GFP

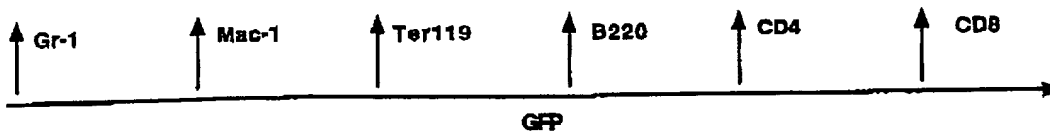
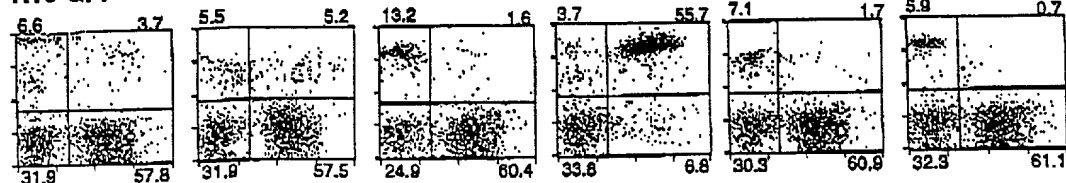
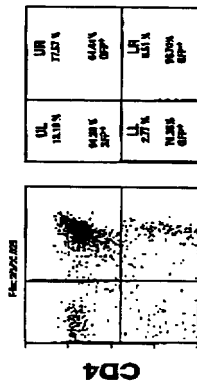
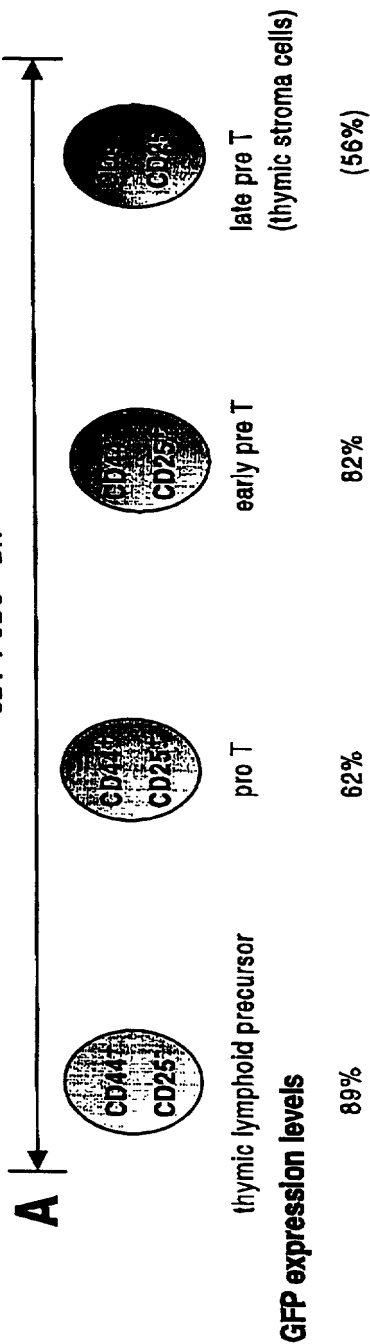


FIG. 12

CD4<sup>+</sup> / CD8<sup>+</sup> DN



CD8

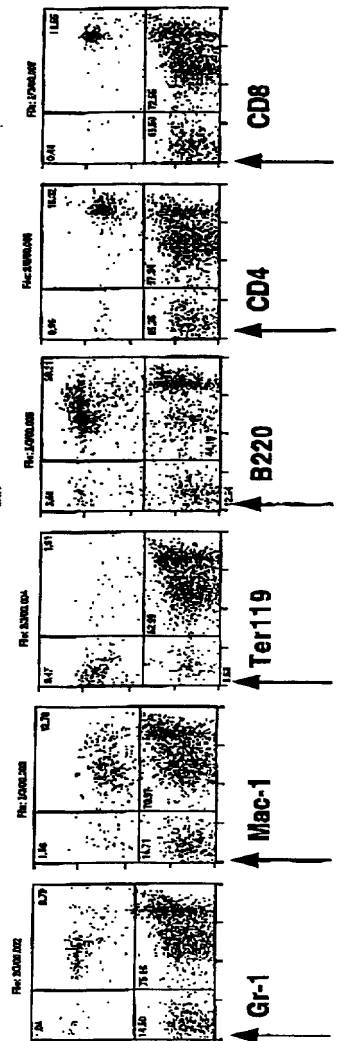
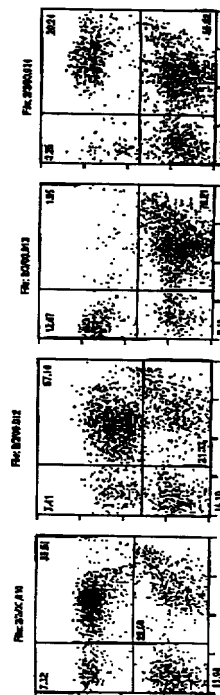


Figure 13